

## SEQUENCE LISTING

<110> Guarente, Leonard P.  
Austriaco Jr., Nicanor  
Claus, James J.  
Cole, Francesca  
Kennedy, Brian

<120> GENES DETERMINING CELLULAR SENESCENCE IN  
YEAST

<130> 0050.1491-005

<150> US 08/396,001

<151> 1995-02-28

<150> PCT/US94/09351

<151> 1994-08-15

<150> US 08/107,408

<151> 1993-08-16

<150> US 09/323,433

<151> 1999-06-01

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gaaaaaagca gacaaaacaa aatttttcct ttttttcgcc tttgtttctc ctgattcggg 300
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His	His	Ser	Asp	Asn	His	His	His	Asn	Asp	Lys	Arg	Ala	Val	Val	Thr	
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Thr	Thr	Ala	Thr	Ser	Ala	Ala	Ala	Asp	Gly	Lys	Val	Glu	Ser	Val	Ala	
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Gln Phe Ile Ser Ser Thr Gln Ser Pro Leu Ala Leu Met Asn Asn Thr  
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Ser Asn Gln Tyr Ala Gln Asp Gln Lys Ile His Ser Pro Gln Gln Ile	
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Met Asn Phe Asn Gln Asn Ala Tyr Pro Ser Met Gly Ala Pro Ser Phe	
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Phe Asp Asn Arg Gln Phe Ala Asn Leu Met Ala His Pro Asn Ser Ala	
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Ala Pro Ile His Ser Phe Ser Ser Ser Asn Ile Thr Asn Val Asn Pro	
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Asn Val Ser Arg Gly Phe Lys Gln Pro Gly Phe Met Met Asn Glu Thr	
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Asp Lys Ile Asn Ala Asn His Phe Ser Pro Tyr Ser Asn Ala Asn Ser	
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Gln Asn Phe Asn Glu Ser Phe Val Pro Arg Met Gln Tyr Gln Thr Glu	
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Gly Ala Asn Trp Asp Ser Ser Leu Ser Met Lys Ser Gln His Ile Gly	
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Gln Gly Pro Tyr Asn Gln Val Asn Met Ser Arg Asn Ala Ser Ile Ser	
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Thr Leu Pro	



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&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 4

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Phe Ile Ser Ser Thr Gln Ser Pro Leu Ala Leu Met Asn Asn Thr Ser
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Asn Ser Thr Gly Leu Ser Ala Ser Met Ala Asn Pro Pro Ala Ile Leu
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Gln Lys Cys Ile Phe Lys Phe Ser Pro Ser Lys Phe Gly Phe Ile Ile
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&lt;211&gt; 888

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

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Asn Met Pro Val Val Leu Thr Ser Gly Thr Gly Ser Gln Ala Gln Pro
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Val Pro Gly Ser Ile Gly Val Ala Gly Arg Ser Gln Asp Asp Ala Met
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Val Asp Tyr Phe Phe Gln Arg Gln His Gly Glu Gln Leu Gly Gly Gly
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Asn His Asp Phe Gln Ala Leu Ala Leu Glu Gly Arg Ala Met Gly Glu
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Arg Pro Gly Gln Ser Phe His Val Asn Ser Glu Val Asn Ser Val Leu
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Val	Leu	Gln	Lys	Gly	Asp	Gly	Asn	Ala	His	Ser	Lys	Lys	Asp	Thr	Glu	
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Tyr	Leu	Gln	Glu	His	Ala	Gln	Glu	Val	Val	Leu	Asp	Lys	Ser	Ala	Cys	
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 Lys Gly Ile Glu Ile Leu Leu Glu Lys Leu Ser Thr  
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tatgagagga tcttttgacg gcaaatagat gcgccatctc cgagaaaaaa tctagacaat 180  
 aacagcgaca attaacctaa agaggataga agatcgagca aaaaaatttt ttaatatggg 240  
 gtcagtggcg atattatact ataggagtta aagagtaagt tgagtgtgta gtggtagaat 300  
 tatgattgaa ctccgaaact aagcgccgat tatgggtggc aaagcggaca gcttttgata 360  
 tataatcgat cgctctcgta gttgatatcc tctctcttgc ttatcttttc ctgtatatag 420  
 tataatgtgta catacagata cgaatatacc tcagtttagt tgttttaaca ttaaataattc 480  
 aacagttgcc agtagcaaaa agaataatc cattcatttc gagctttttc gtctcattac 540  
 tgatatccaa ctaacagtct cctcatagac ggtaccttac tttcctttaa tattaaaata 600  
 ctagtatagt cgcacatact taactcgtct ctctctaaca cata atg aaa att tcc 656

Met Lys Ile Ser

1

gca gct tta ata ttg tct tcc ctt tct tct gtc gca ttt tct gcc cct 704  
 Ala Ala Leu Ile Leu Ser Ser Leu Ser Ser Val Ala Phe Ser Ala Pro  
 5 10 15 20

gca cct gct cca gcg gac agt cat cat gaa gat cat cac aaa gat gaa 752  
 Ala Pro Ala Pro Ala Asp Ser His His Glu Asp His His Lys Asp Glu  
 25 30 35

aaa cca gcg gtt gtc act gtc act caa tac ata gat tcc aat gcc gct 800  
 Lys Pro Ala Val Val Thr Val Thr Gln Tyr Ile Asp Ser Asn Ala Ala  
 40 45 50

act agt act gta gaa tct gct gct act acc act aca ttg tcc tca tct 848  
 Thr Ser Thr Val Glu Ser Ala Ala Thr Thr Thr Thr Leu Ser Ser Ser  
 55 60 65

gag aag gat acc tct gaa cag aag cgt gat ggc gga ttc caa gat ggt 896  
 Glu Lys Asp Thr Ser Glu Gln Lys Arg Asp Gly Gly Phe Gln Asp Gly  
 70 75 80

act gtc aaa tgt tct gac ttc cct tct gta aac ggt ata gtt tcc ttg 944  
 Thr Val Lys Cys Ser Asp Phe Pro Ser Val Asn Gly Ile Val Ser Leu  
 85 90 95 100

gac tgg cta gga ttt ggt gga tgg gcc tct gtc atg gac atg gat gcc 992  
 Asp Trp Leu Gly Phe Gly Gly Trp Ala Ser Val Met Asp Met Asp Ala  
 105 110 115

aac act tcg tcc gaa tgt aag gat ggc tac tac tgt tct tat gca tgt 1040  
 Asn Thr Ser Ser Glu Cys Lys Asp Gly Tyr Tyr Cys Ser Tyr Ala Cys  
 120 125 130

gaa cct gga atg tca aag act caa tgg cct tct gac caa cca agc gat 1088  
 Glu Pro Gly Met Ser Lys Thr Gln Trp Pro Ser Asp Gln Pro Ser Asp  
 135 140 145

ggt aaa tct gtt ggt ggt ctt tat tgt aaa aat ggt tac ttg tac cgt 1136  
 Gly Lys Ser Val Gly Gly Leu Tyr Cys Lys Asn Gly Tyr Leu Tyr Arg  
 150 155 160

acc aac act gat acc agc gat tta tgt tct acg gat gaa aca tct gct 1184  
 Thr Asn Thr Asp Thr Ser Asp Leu Cys Ser Thr Asp Glu Thr Ser Ala  
 165 170 175 180

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 185 190 195

tac cca gga tct gaa aac atg gtg att ccc aca gtg gtt gat ggt gga 1280  
Tyr Pro Gly Ser Glu Asn Met Val Ile Pro Thr Val Val Asp Gly Gly  
200 205 210

gat tca caa cca att tca gtc gtt gat gaa gac act tat tat caa tgg 1328  
Asp Ser Gln Pro Ile Ser Val Val Asp Glu Asp Thr Tyr Tyr Gln Trp  
215 220 225

cag ggt aaa aag act tct gct cag tac tat att aac aac gcc ggt gta 1376  
Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Ile Asn Asn Ala Gly Val  
230 235 240

tct gca gaa gat ggg tgc att tgg ggt act tct ggt tcg gat gtc ggc 1424  
Ser Ala Glu Asp Gly Cys Ile Trp Gly Thr Ser Gly Ser Asp Val Gly  
245 250 255 260

aac tgg gct cca cta gtg tta ggt gct ggt tcc act aat gga gaa aca 1472  
Asn Trp Ala Pro Leu Val Leu Gly Ala Gly Ser Thr Asn Gly Glu Thr  
265 270 275

tac ttg tcg ttg att cca aac ccc aac agt aac caa gct gcc aac ttt 1520  
Tyr Leu Ser Leu Ile Pro Asn Pro Asn Ser Asn Gln Ala Ala Asn Phe  
280 285 290

aac gtt aaa ata gtt gca tcc gat ggc gct aac gtt cag ggc agc tgt 1568  
Asn Val Lys Ile Val Ala Ser Asp Gly Ala Asn Val Gln Gly Ser Cys  
295 300 305

gcg tat gaa gat ggc tct ttc acc gga gat ggt tcc gat ggt tgc aca 1616  
Ala Tyr Glu Asp Gly Ser Phe Thr Gly Asp Gly Ser Asp Gly Cys Thr  
310 315 320

gtt tct gtt tta tct gga tct gct gaa ttt gtt ttc tat taagtcactc 1665  
Val Ser Val Leu Ser Gly Ser Ala Glu Phe Val Phe Tyr  
325 330 335

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cgacaacca cagtagtaac actcatgact aaattttcat cagtacttaa tgtcatgtta 2385  
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<211> 337

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 12

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 20 25 30  
 His Lys Asp Glu Lys Pro Ala Val Val Thr Val Thr Gln Tyr Ile Asp  
 35 40 45  
 Ser Asn Ala Ala Thr Ser Thr Val Glu Ser Ala Ala Thr Thr Thr Thr  
 50 55 60  
 Leu Ser Ser Ser Glu Lys Asp Thr Ser Glu Gln Lys Arg Asp Gly Gly  
 65 70 75 80  
 Phe Gln Asp Gly Thr Val Lys Cys Ser Asp Phe Pro Ser Val Asn Gly  
 85 90 95  
 Ile Val Ser Leu Asp Trp Leu Gly Phe Gly Gly Trp Ala Ser Val Met  
 100 105 110  
 Asp Met Asp Ala Asn Thr Ser Ser Glu Cys Lys Asp Gly Tyr Tyr Cys  
 115 120 125  
 Ser Tyr Ala Cys Glu Pro Gly Met Ser Lys Thr Gln Trp Pro Ser Asp  
 130 135 140  
 Gln Pro Ser Asp Gly Lys Ser Val Gly Gly Leu Tyr Cys Lys Asn Gly  
 145 150 155 160  
 Tyr Leu Tyr Arg Thr Asn Thr Asp Thr Ser Asp Leu Cys Ser Thr Asp  
 165 170 175  
 Glu Thr Ser Ala Lys Ala Ile Asn Lys Lys Ser Asp Ser Ile Ala Leu  
 180 185 190  
 Cys Arg Thr Asp Tyr Pro Gly Ser Glu Asn Met Val Ile Pro Thr Val  
 195 200 205  
 Val Asp Gly Gly Asp Ser Gln Pro Ile Ser Val Val Asp Glu Asp Thr  
 210 215 220  
 Tyr Tyr Gln Trp Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Ile Asn  
 225 230 235 240  
 Asn Ala Gly Val Ser Ala Glu Asp Gly Cys Ile Trp Gly Thr Ser Gly  
 245 250 255  
 Ser Asp Val Gly Asn Trp Ala Pro Leu Val Leu Gly Ala Gly Ser Thr  
 260 265 270  
 Asn Gly Glu Thr Tyr Leu Ser Leu Ile Pro Asn Pro Asn Ser Asn Gln  
 275 280 285  
 Ala Ala Asn Phe Asn Val Lys Ile Val Ala Ser Asp Gly Ala Asn Val  
 290 295 300  
 Gln Gly Ser Cys Ala Tyr Glu Asp Gly Ser Phe Thr Gly Asp Gly Ser  
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 Asp Gly Cys Thr Val Ser Val Leu Ser Gly Ser Ala Glu Phe Val Phe  
 325 330 335  
 Tyr

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 tgccatgaat accaaggcgt gctcagcttc tgcagcagtt caaccctttc caataccgcc 180



aatgcgtcct caaaacgtta gtttagtcgt gctcaaccgc tatttttgggt tttatcttcg 240  
 tttcttttctc ctgaacgaca ttcgtcacga aaattgcggc ggaaaatttc ctgatgcgga 300  
 cactttttcc cgatccggac atgccttttt ttggcgtttc gcgtcagtca atagaagttt 360  
 cagatctaca ttaggaagaa ccagaaaata gccattaatg ctttcagcat agcacagcat 420  
 agcagctgtg tatatcttaa ataagatgta gactggtttg catttggaag ggttttgtgt 480  
 aagaaaagca atacttgagg taaaacaaga gaaaaaaaaa cactttacta actaatatcc 540  
 aatcctttat ttttttgcag aa atg aaa ttc tca act gcc gtt act acg ttg 592  
 Met Lys Phe Ser Thr Ala Val Thr Thr Leu  
 1 5 10

att agt tct ggt gcc atc gtg tct gct tta cca cac gtg gat gtt cac 640  
 Ile Ser Ser Gly Ala Ile Val Ser Ala Leu Pro His Val Asp Val His  
 15 20 25

caa gaa gat gcc cac caa cat aag agg gcc gtt gcg tac aaa tac gtt 688  
 Gln Glu Asp Ala His Gln His Lys Arg Ala Val Ala Tyr Lys Tyr Val  
 30 35 40

tac gaa act gtt gtt gtc gat tct gat ggc cac act gta act cct gct 736  
 Tyr Glu Thr Val Val Val Asp Ser Asp Gly His Thr Val Thr Pro Ala  
 45 50 55

gct tca gaa gtc gct act gct gct acc tct gct atc att aca aca tct 784  
 Ala Ser Glu Val Ala Thr Ala Ala Thr Ser Ala Ile Ile Thr Thr Ser  
 60 65 70

gtg ttg gct cca acc tcc tcc gca gcc gct ggg ata gcc gct tcc att 832  
 Val Leu Ala Pro Thr Ser Ser Ala Ala Ala Gly Ile Ala Ala Ser Ile  
 75 80 85 90

gct gtt tca tct gct gcc tta gcc aag aat gag aaa atc tct gat gcc 880  
 Ala Val Ser Ser Ala Ala Leu Ala Lys Asn Glu Lys Ile Ser Asp Ala  
 95 100 105

gct gca tct gcc act gcc tca aca tct caa ggg gca tcc tcc tcc tcc 928  
 Ala Ala Ser Ala Thr Ala Ser Thr Ser Gln Gly Ala Ser Ser Ser Ser  
 110 115 120

tcc tcc tcc tcg gca act tct acc cta gaa agc agc tct gtt tct tca 976  
 Ser Ser Ser Ser Ala Thr Ser Thr Leu Glu Ser Ser Ser Val Ser Ser  
 125 130 135

tct agt gaa gaa gct gct cca aca tct act gtc gtg tca act tct tcc 1024  
 Ser Ser Glu Glu Ala Ala Pro Thr Ser Thr Val Val Ser Thr Ser Ser  
 140 145 150

gca acc caa tct agt gct tct tct gcc act aaa tct agt act tct tcc 1072  
 Ala Thr Gln Ser Ser Ala Ser Ser Ala Thr Lys Ser Ser Thr Ser Ser  
 155 160 165 170

act tca cca tct act tct act tct act tcc act tct tct act tcc tct 1120  
 Thr Ser Pro Ser Thr Ser Thr Ser Thr Ser Thr Ser Ser Thr Ser Ser  
 175 180 185

tcc tct tcc tcc tcc tcc tcc tct tct tct tct tct tct ggc agt ggt 1168  
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly Ser Gly  
 190 195 200

agt atc tac ggt gat ttg gcc gac ttt tca ggc cca agt gag aaa ttc 1216

Ser	Ile	Tyr	Gly	Asp	Leu	Ala	Asp	Phe	Ser	Gly	Pro	Ser	Glu	Lys	Phe		
		205					210					215					
caa	gac	ggc	act	att	cca	tgt	gac	aaa	ttc	cca	tct	ggg	caa	ggg	gtc	1264	
Gln	Asp	Gly	Thr	Ile	Pro	Cys	Asp	Lys	Phe	Pro	Ser	Gly	Gln	Gly	Val		
	220					225				230							
att	tct	att	gac	tgg	att	ggc	gag	ggg	gga	tgg	tcc	ggg	gtg	gaa	aac	1312	
Ile	Ser	Ile	Asp	Trp	Ile	Gly	Glu	Gly	Gly	Trp	Ser	Gly	Val	Glu	Asn		
235					240					245					250		
acc	gac	act	tcc	act	ggc	ggg	tca	tgc	aag	gag	ggg	tcc	tac	tgt	tcc	1360	
Thr	Asp	Thr	Ser	Thr	Gly	Gly	Ser	Cys	Lys	Glu	Gly	Ser	Tyr	Cys	Ser		
				255					260					265			
tac	tcc	tgc	caa	cca	ggg	atg	tct	aag	acc	caa	tgg	cca	tcc	gat	caa	1408	
Tyr	Ser	Cys	Gln	Pro	Gly	Met	Ser	Lys	Thr	Gln	Trp	Pro	Ser	Asp	Gln		
			270					275					280				
cca	tct	gac	ggg	aga	tct	gtc	ggg	ggg	ttg	ttg	tgt	aaa	aat	ggg	tat	1456	
Pro	Ser	Asp	Gly	Arg	Ser	Val	Gly	Gly	Leu	Leu	Cys	Lys	Asn	Gly	Tyr		
		285					290					295					
ttg	tac	cgt	tct	aac	act	gac	gcg	gat	tac	tta	tgt	gaa	tgg	ggg	gtc	1504	
Leu	Tyr	Arg	Ser	Asn	Thr	Asp	Ala	Asp	Tyr	Leu	Cys	Glu	Trp	Gly	Val		
	300					305					310						
gag	gct	gcc	tat	gtt	gtt	tct	aaa	cta	agc	aag	ggg	gtc	gcc	att	tgc	1552	
Glu	Ala	Ala	Tyr	Val	Val	Ser	Lys	Leu	Ser	Lys	Gly	Val	Ala	Ile	Cys		
	315				320					325					330		
aga	acc	gac	tac	ccg	ggc	act	gaa	aac	atg	gtt	atc	cca	acc	tat	gtt	1600	
Arg	Thr	Asp	Tyr	Pro	Gly	Thr	Glu	Asn	Met	Val	Ile	Pro	Thr	Tyr	Val		
				335					340					345			
gaa	ggg	ggg	agc	tct	ttg	cca	ttg	acc	gtt	gtt	gac	caa	gat	act	tac	1648	
Glu	Gly	Gly	Ser	Ser	Leu	Pro	Leu	Thr	Val	Val	Asp	Gln	Asp	Thr	Tyr		
			350					355					360				
ttt	act	tgg	gaa	ggc	aaa	aag	aca	tct	gct	caa	tac	tac	gtt	aat	aac	1696	
Phe	Thr	Trp	Glu	Gly	Lys	Lys	Thr	Ser	Ala	Gln	Tyr	Tyr	Val	Asn	Asn		
		365					370					375					
gcc	ggc	gtc	tca	gtt	gaa	gat	ggg	tgt	atc	tgg	ggg	act	tct	gga	tct	1744	
Ala	Gly	Val	Ser	Val	Glu	Asp	Gly	Cys	Ile	Trp	Gly	Thr	Ser	Gly	Ser		
	380					385					390						
ggg	att	ggg	aac	tgg	gca	cca	tta	aac	ttt	ggg	gct	ggc	tcc	act	ggg	1792	
Gly	Ile	Gly	Asn	Trp	Ala	Pro	Leu	Asn	Phe	Gly	Ala	Gly	Ser	Thr	Gly		
	395				400					405					410		
gga	gtg	aca	tac	tta	tca	ttg	att	cct	aac	cca	aac	aac	agc	gac	gca	1840	
Gly	Val	Thr	Tyr	Leu	Ser	Leu	Ile	Pro	Asn	Pro	Asn	Asn	Ser	Asp	Ala		
				415					420					425			
ttg	aac	tac	aac	gtc	aag	ata	gtt	gct	gct	gat	gat	tca	tcc	aat	gtc	1888	
Leu	Asn	Tyr	Asn	Val	Lys	Ile	Val	Ala	Ala	Asp	Asp	Ser	Ser	Asn	Val		
			430					435					440				

atc ggt gaa tgt gtt tac gaa aat ggt gag ttc tct ggc ggt gct gac 1936  
 Ile Gly Glu Cys Val Tyr Glu Asn Gly Glu Phe Ser Gly Gly Ala Asp  
           445                                  450                                  455

ggg tgt acc gtc tct gtt act tcc ggt aaa gct cat ttc gtc tta tac 1984  
 Gly Cys Thr Val Ser Val Thr Ser Gly Lys Ala His Phe Val Leu Tyr  
           460                                  465                                  470

aat taagctacgt gactactact tttccttttt tttttctttt ttcgaacaca 2037  
 Asn  
 475

tctcaccccc tatacctcac acaatcacta tgggtccctt ttcttttttac cgatatttat 2097  
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<211> 475

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 14

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           20                                  25                                  30  
 His Lys Arg Ala Val Ala Tyr Lys Tyr Val Tyr Glu Thr Val Val Val  
           35                                  40                                  45  
 Asp Ser Asp Gly His Thr Val Thr Pro Ala Ala Ser Glu Val Ala Thr  
           50                                  55                                  60  
 Ala Ala Thr Ser Ala Ile Ile Thr Thr Ser Val Leu Ala Pro Thr Ser  
           65                                  70                                  75                                  80  
 Ser Ala Ala Ala Gly Ile Ala Ala Ser Ile Ala Val Ser Ser Ala Ala  
           85                                  90                                  95  
 Leu Ala Lys Asn Glu Lys Ile Ser Asp Ala Ala Ala Ser Ala Thr Ala  
           100                                  105                                  110  
 Ser Thr Ser Gln Gly Ala Ser Ser Ser Ser Ser Ser Ser Ser Ala Thr  
           115                                  120                                  125  
 Ser Thr Leu Glu Ser Ser Ser Val Ser Ser Ser Ser Glu Glu Ala Ala  
           130                                  135                                  140  
 Pro Thr Ser Thr Val Val Ser Thr Ser Ser Ala Thr Gln Ser Ser Ala  
           145                                  150                                  155                                  160  
 Ser Ser Ala Thr Lys Ser Ser Thr Ser Ser Thr Ser Pro Ser Thr Ser  
           165                                  170                                  175  
 Thr Ser Thr Ser Thr Ser Ser Thr Ser Ser Ser Ser Ser Ser Ser Ser  
           180                                  185                                  190  
 Ser Ser Ser Ser Ser Ser Ser Gly Ser Gly Ser Ile Tyr Gly Asp Leu  
           195                                  200                                  205  
 Ala Asp Phe Ser Gly Pro Ser Glu Lys Phe Gln Asp Gly Thr Ile Pro  
           210                                  215                                  220  
 Cys Asp Lys Phe Pro Ser Gly Gln Gly Val Ile Ser Ile Asp Trp Ile  
           225                                  230                                  235                                  240  
 Gly Glu Gly Gly Trp Ser Gly Val Glu Asn Thr Asp Thr Ser Thr Gly  
           245                                  250                                  255  
 Gly Ser Cys Lys Glu Gly Ser Tyr Cys Ser Tyr Ser Cys Gln Pro Gly  
           260                                  265                                  270  
 Met Ser Lys Thr Gln Trp Pro Ser Asp Gln Pro Ser Asp Gly Arg Ser  
           275                                  280                                  285  
 Val Gly Gly Leu Leu Cys Lys Asn Gly Tyr Leu Tyr Arg Ser Asn Thr  
           290                                  295                                  300

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Asp Ala Asp Tyr Leu Cys Glu Trp Gly Val Glu Ala Ala Tyr Val Val
305          310          315          320
Ser Lys Leu Ser Lys Gly Val Ala Ile Cys Arg Thr Asp Tyr Pro Gly
          325          330          335
Thr Glu Asn Met Val Ile Pro Thr Tyr Val Glu Gly Gly Ser Ser Leu
          340          345          350
Pro Leu Thr Val Val Asp Gln Asp Thr Tyr Phe Thr Trp Glu Gly Lys
          355          360          365
Lys Thr Ser Ala Gln Tyr Tyr Val Asn Asn Ala Gly Val Ser Val Glu
          370          375          380
Asp Gly Cys Ile Trp Gly Thr Ser Gly Ser Gly Ile Gly Asn Trp Ala
385          390          395          400
Pro Leu Asn Phe Gly Ala Gly Ser Thr Gly Gly Val Thr Tyr Leu Ser
          405          410          415
Leu Ile Pro Asn Pro Asn Asn Ser Asp Ala Leu Asn Tyr Asn Val Lys
          420          425          430
Ile Val Ala Ala Asp Asp Ser Ser Asn Val Ile Gly Glu Cys Val Tyr
          435          440          445
Glu Asn Gly Glu Phe Ser Gly Gly Ala Asp Gly Cys Thr Val Ser Val
          450          455          460
Thr Ser Gly Lys Ala His Phe Val Leu Tyr Asn
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<210> 15
<211> 145
<212> PRT
<213> Saccharomyces cerevisiae

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          20      25      30
Xaa Trp Xaa Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Xaa Asn Asn Xaa
          35      40      45
Gly Val Ser Xaa Glu Asp Gly Cys Ile Trp Gly Thr Xaa Gly Ser Xaa
50      55      60
Xaa Gly Asn Trp Ala Pro Xaa Xaa Xaa Gly Ala Xaa Xaa Thr Xaa Gly
65      70      75      80
Xaa Thr Tyr Leu Ser Xaa Ile Pro Asn Pro Asn Xaa Xaa Xaa Ala Xaa
          85      90      95
Asn Xaa Asn Xaa Lys Ile Val Ala Xaa Asp Xaa Xaa Xaa Xaa Val Xaa
          100     105     110
Gly Xaa Cys Xaa Tyr Glu Xaa Gly Xaa Xaa Xaa Gly Xaa Gly Xaa Asp
          115     120     125
Gly Cys Thr Val Ser Val Xaa Ser Gly Xaa Ala Xaa Phe Val Xaa Tyr
130      135      140
Xaa
145

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<210> 16
<211> 60

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&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 16

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Ser Leu Ile Pro Asn Pro Asn Asn Gly Asn Ala Leu Asn Phe Asn Val
 1             5             10             15
Lys Ile Val Ala Ala Asp Asp Ser Ser Thr Val Asn Gly Glu Cys Ile
          20             25             30
Tyr Glu Asn Gly Ser Phe Ser Ser Gly Gly Ser Asp Gly Cys Thr Val
      35             40             45
Ser Val Thr Ala Gly Lys Ala Lys Phe Val Leu Tyr
 50             55             60

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&lt;210&gt; 17

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 17

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Leu Ala Thr Asp Gln Phe Gly Cys Arg Phe Leu Gln Lys Lys Leu Glu
 1             5             10             15

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&lt;210&gt; 18

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 18

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Leu Ile Leu Asp Pro Phe Gly Asn Tyr Leu Val Asp Lys Ile Cys Asp
 1             5             10             15

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&lt;210&gt; 19

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 19

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Ile Ser Ile Asn Gln Tyr Gly Thr Arg Ser Leu Gln Lys Ile Ile Asp
 1             5             10             15

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&lt;210&gt; 20

&lt;211&gt; 15

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 20

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Leu Ile Asn Asp Ile Asn Gly His Val Ile Gln Lys Cys Ile Phe
 1             5             10             15

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&lt;210&gt; 21

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 21

Ile	Ser	Thr	His	Lys	His	Gly	Cys	Cys	Val	Leu	Gln	Lys	Ile	Leu	Ser
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&lt;210&gt; 22

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 22

Leu	Ile	Asn	Asp	Gln	Phe	Gly	Asn	Tyr	Ile	Ile	Gln	Phe	Ile	Leu	Asp
1				5					10					15	

&lt;210&gt; 23

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 23

Leu	Ser	Cys	Leu	Lys	Phe	Ser	Ser	Asn	Val	Val	Glu	Lys	Phe	Ile	Lys
1				5					10					15	

&lt;210&gt; 24

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 24

Leu	Ile	Arg	Asp	Asn	Phe	Gly	Asn	Tyr	Ala	Leu	Gln	Thr	Leu	Leu	Asp
1				5					10					15	

&lt;210&gt; 25

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 25

Leu	Cys	Lys	Asp	Gln	His	Gly	Cys	Arg	Phe	Leu	Gln	Lys	Gln	Leu	Asp
1				5					10					15	

&lt;210&gt; 26

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 26

Leu	Met	Thr	Asp	Ser	Phe	Gly	Asn	Tyr	Leu	Ile	Gln	Lys	Leu	Leu	Glu
1				5					10					15	

&lt;210&gt; 27

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 27

Ile	Ser	Leu	Asn	Pro	His	Gly	Thr	Arg	Ala	Leu	Gln	Lys	Leu	Ile	Glu
1				5					10					15	

&lt;210&gt; 28

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 28

Leu	Ser	Lys	Asp	Leu	Asn	Gly	Asn	His	Val	Ile	Gln	Lys	Cys	Leu	Gln
1				5					10					15	

&lt;210&gt; 29

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 29

Ile	Ala	Thr	His	Arg	His	Gly	Cys	Cys	Val	Leu	Gln	Arg	Cys	Leu	Asp
1				5					10					15	

&lt;210&gt; 30

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 30

Leu	Thr	Leu	Asp	Pro	Phe	Gly	Asn	Tyr	Val	Val	Gln	Tyr	Ile	Ile	Thr
1				5					10					15	

&lt;210&gt; 31

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 31

Leu	Ser	Ile	His	Lys	Phe	Gly	Ser	Asn	Val	Ile	Glu	Lys	Ile	Ile	Lys
1				5					10					15	

&lt;210&gt; 32

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 32

Leu	Leu	Asn	Asp	Ser	Tyr	Gly	Asn	Tyr	Val	Leu	Gln	Thr	Ala	Leu	Asp
1				5					10					15	

&lt;210&gt; 33

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Drosophila*

&lt;400&gt; 33

Phe	Ser	Gln	Asp	Gln	His	Gly	Ser	Arg	Phe	Ile	Gln	Gln	Lys	Leu	Glu
1				5					10					15	

&lt;210&gt; 34

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Drosophila

&lt;400&gt; 34

Leu	Met	Thr	Asp	Val	Phe	Gly	Asn	Tyr	Val	Ile	Gln	Lys	Phe	Phe	Glu
1				5					10					15	

&lt;210&gt; 35

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Drosophila

&lt;400&gt; 35

Leu	Ala	Leu	Gln	Met	Tyr	Gly	Leu	Arg	Val	Ile	Gln	Lys	Ala	Leu	Glu
1				5					10					15	

&lt;210&gt; 36

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Drosophila

&lt;400&gt; 36

Cys	Val	Lys	Asp	Gln	Asn	Gly	Asn	His	Val	Val	Gln	Lys	Cys	Ile	Glu
1				5					10					15	

&lt;210&gt; 37

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Drosophila

&lt;400&gt; 37

Leu	Ser	Thr	His	Pro	Tyr	Gly	Cys	Arg	Val	Ile	Gln	Arg	Ile	Leu	Glu
1				5					10					15	

&lt;210&gt; 38

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Drosophila

&lt;400&gt; 38

Leu	Ile	Gln	Asp	Gln	Tyr	Gly	Asn	Tyr	Val	Ile	Gln	His	Val	Leu	Glu
1				5					10					15	

&lt;210&gt; 39

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Drosophila



&lt;400&gt; 39

Leu	Ser	Gln	His	Lys	Phe	Ala	Ser	Asn	Val	Val	Glu	Lys	Cys	Val	Thr
1				5					10					15	

&lt;210&gt; 40

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Drosophila

&lt;400&gt; 40

Met	Met	Lys	Asp	Gln	Tyr	Ala	Asn	Tyr	Val	Val	Gln	Lys	Met	Ile	Asp
1				5					10					15	

&lt;210&gt; 41

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 41

Phe	Ser	Gln	Asp	Gln	His	Gly	Ser	Arg	Phe	Ile	Gln	Leu	Lys	Leu	Glu
1				5					10					15	

&lt;210&gt; 42

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

Leu	Met	Arg	Asp	Val	Phe	Gly	Asn	Tyr	Val	Ile	Gln	Lys	Phe	Phe	Glu
1				5					10					15	

&lt;210&gt; 43

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

Leu	Ala	Leu	Gln	Met	Tyr	Gly	Leu	Arg	Val	Ile	Gln	Lys	Ala	Leu	Glu
1				5					10					15	

&lt;210&gt; 44

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

Cys	Val	Lys	Asp	Gln	Asn	Gly	Asn	His	Val	Val	Gln	Lys	Cys	Ile	Glu
1				5					10					15	

&lt;210&gt; 45

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

Leu	Ser	Thr	His	Pro	Tyr	Gly	Cys	Arg	Val	Ile	Gln	Arg	Ile	Leu	Glu
1				5					10					15	

&lt;210&gt; 46

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

Leu	Val	Gln	Asp	Gln	Tyr	Gly	Asn	Tyr	Val	Ile	Gln	His	Val	Leu	Glu
1				5					10					15	

&lt;210&gt; 47

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

Val	Leu	Ser	Gln	His	Phe	Ala	Ser	Asn	Val	Val	Glu	Lys	Cys	Val	Thr
1				5					10					15	

&lt;210&gt; 48

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

Met	Met	Lys	Asp	Gln	Tyr	Ala	Asn	Tyr	Val	Val	Gln	Lys	Met	Ile	Asp
1				5					10					15	